



O.G. FIG.	
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CLASS	SUBCLASS

1 TCAAGAGCGCCTCGGGGTACCATGGGGAGCGGATCGGGGCCCCGCAAGGGCGGAGGGGGCCCCGAAGGACTTCGGCGC
M G S D R A R K G G G G P K D F G A 18

76 GGGACTCAAGTACAACCTCCCGCAGAGAAAGTGAATGGCTTGAGGAAGCGGTGGAGTTCTCCAGTCAACAA
G L K Y N S R H E K V N G L E E G V E F L P V N N 43

151 CGTCAAGAAGTGGAAGCATGGCCCCGGGGCGTGGTGGTGGCTGGCAGCCCGTGTGATCGGCCCTCCTCTTGGT
V K K V E K H G P G R W V V L A A V L I G L L L V 68

226 CTTGCTGGGATCGGCTTCCCTGGTGTGGCATTTGCAGTACCGGGACGTGCTGCCAGAGGCTCTCAATGGCTA
L L G I G F L V W H L Q Y R D V R V Q K V F N G Y 93

301 CATGAGGATCACAATGAGAAATTTGTGGATGCCCTACGAGAACTCCAACCTCCACTGAGTTTGTAAAGCCTGGCCAG
M R I T N E N F V D A Y E N S N S T E F V S L A S 118

376 CAAGGTGAAGGACGCGCTGAAGCTGCTGTACAGCGGAGTCCCATTCCTGGCCCCCTACCACAAGGAGTCGGCTGT
K V K D A L K L L Y S G V P F L G P Y H K E S A V 143

451 GACGGCCTTCAGCGAGGCGGTCATCGCCCTACTACTGGTCTGAGTTCAGCATCCCGCAGCACCTGGTGGAGGA
T A F S E G S V I A Y Y W S E F S I P Q H L V E E 168

526 GGCCGAGCGGTGATGGCCGAGGAGCGGTAGTCATGCTGCCCCCGGGCGCTCCCTGAAAGTCCCTTTGTGGT
A E R V M A E E R V V M L P P R A R S L K S F V V 193

601 CACCTCAGTGGTGGCTTTCCCCACGGACTCCAAAACAGTACAGAGGACCCAGGACAACAGCTGCAGCTTTGGCCT
T S V V A F P T D S K T V Q R T Q D N S C S F G L 218

676 GCACGCCCGGTGTGGAGCTGATGCGCTTCACCACGCCCGGCTTCCCTGACAGCCCCCTACCCCGCTCATGCCCG
H A R G V E L M R G T T P G R P D S P Y P A H A R 243

Fig. 2A

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DRAFTSMAN	CLASS	SUBCLASS



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751 CTGCCAGTGGCCCTGCGGGGACGCCGACTCAGTGTGAGCCTCACCCTTCCGCAGCTTTGACCTTGCGTCCCTG
   C Q W A L R G D A D S V L S L T F R S F D L A S C 268
826 CGACGAGCGCGGACCGTGTGACGGTGTACAACACCTTGAGCCCATGAGCCCCACGCCCTGGTGCAGTT
   D E R G S D L V T V Y N T L S P M E P H A L V Q L 293
901 GTGTGGCACCTACCTCCCTCCTACAACCTGACCTTCCACTCCTCCAGAACGTCTGCTCATCACACTGATAAC
   C G T Y P P S Y N L T F H S S Q N V L L I T L I T 318
976 CAACACTGAGCGGCGCATCCCGGCTTTGAGGCCACCTTCTTCCAGCTGCCCTAGGATGAGCAGCTGTGGAGCGCG
   N T E F F H P G F E A T F F Q L P R M S S C G G R 343
1051 CTTACGTAAAGCCAGGGGACATTCAACAGCCCCCTACTACCCAGGCCACTACCCACCCCAACATTGACTGCACATG
   L R K A Q G T F N S P Y Y P G H Y P P N I D C T W 368
1126 GAACATTGAGGTGCCCAACACAGCATGTGAAGGTGAGCTTCAAAATTCTTCTACCTGCTGGAGCCCGCGTGCC
   N I E V P N N Q H V K V S F K F F Y L L E P G V P 393
1201 TGCGGGCACCTGCCCCAAGGACTACGTGGAGATCAATGGGAGAAATACTCGGAGAGAGGTCCTCCAGTTTCGTCT
   A G T C P K D Y V E I N G E K Y C G E R S Q F V V 418
1276 CACCAGCAACAGCAAGATCACAGTTTCGCTTCCACTCAGATCAGTCTTACACCGACACCCGGCTTCTTAGCTGA
   T S N S N K I T V R F H S D Q S Y T D T G F L A E 443
1351 ATACCTCTCCTACGACTCCAGTGACCCATGCCCCGGGCGAGTTACGTTGCCGCACGGCGGTGTATCCGGAAGGA
   Y L S Y D S S D P C P G Q F T C R T G R C I R K E 468
1426 GCTGCGCTGTGATGGCGCGGACTGCACCCGACACAGCGATGAGCTCAACTGCAGTTGCGACGCGCGGCCACCA
   L R C D G W A D C T D H S D E L N C S C D A G H Q 493

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Fig. 2B

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APPROVED	O.G. FIG.	
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1501 GTTCACGTGCAAGAACAAGTTCTGCAAGCCCCCTCTTCTGGGTCTGCGACAGTGTGAACGACTGCGGAGACAACAG
F T C K N K F C K P L F W V C D S V N D C G D N S 518

1576 CGACGACGAGGGGTGCAGTTGTCCGGCCAGACCTTCAAGTGTCCAATGGGAAGTGCCTCTCGAAAAGCCAGCA
D E Q G C S C P A Q T F R C S N G K C L S K S Q Q 543

1651 GTGCAATGGGAAGGACGACTGTGGGGACGGGTCCGACGAGGCCCTCCTGCCCAAGGTGAACGTCGTCACCTTGTA
C N G K D D C G D G S D E A S C P K V N V V T C T 568

1726 CAAACACACTACCGCTGCCCTCAATGGCTCTGCTTGAGCAAGGCAACCTGAGTGTGACGGGAAGGAGACTG
K H T Y R C L N G L C L S K G N P E C D G K E D C 593

1801 TAGCGACGGCTCAGATGAGAAGGACTGCGACTGTGGGCTGCGGTCTTCAACGACAGAGGCTCGTGTGTTGGGGG
S D G S D E K D C D C G L R S F T R Q A R V V G G 618

1876 CACGGATGCGGATGAGGGGAGTGGCCCTGGCAGGTAAGCCTGCATGCTCTGGGCCAGGGCCACATCTGCGGTGC
T D A D E G E W P W Q V S L H A L G Q G H I C G A 643

1951 TTCCCTCATCTCTCCAACTGGCTGGTCTCTGCCGCACACTGCTACATCGATGACAGAGGATTTCAGGTACTCAGA
S L I S P N W L V S A A H C Y I D D R G F R Y S D 668

2026 CCCCACGAGTGGACGGCCCTTCCCTGGGCTTGACGACCAAGCCAGCGCCCTGGGTGTCAGGAGCGCAG
P T Q W T A F L G L H D Q S Q R S A P G V Q E R R 693

2101 GCTCAAGCGCATCATCTCCACCCCTTCTTCAATGACTTCACTTCCGACTATGACATCGCGCTGCTGGAGCTGGA
L K R I I S H P F F N D F T F D Y D I A L L E L E 718

2176 GAAACCGGACAGTACAGCTCCATGGTGGGCCCATCTGCCTGCCGGACGCCCTCCCATGTCTTCCCTGCCCGCAA
K P A E Y S S M V R P I C L P D A S H V F P A G K 743

Fig. 2C

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APPROVED	O.G. FIG.	
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2251 GGCCATCTGGGTACGGGCTGGGACACACCCAGTATGGAGGCACTGGCGCGCTGATCCTGCAAAAGGTGAGAT
A I W V T G W G H T Q Y G G T G A L I L Q K G E I 768
2326 CCGCGTCATCAACAGACCACTGCGAGAACCTCCTGCCGACAGATCACGCCGCGCATGATGTGCGTGGCCTT
R V I N Q T T C E N L L P Q Q I T P R M C V G F 793
2401 CCTCAGCGCGGCTGGACTCCTGCCAGGGTGATTCGGGGGACCCCTGTCCAGCGTGGAGGCGGATGGGCGGAT
L S G G V D S C Q G D S G G P L S S V E A D G R I 818
2476 CTTCCAGGCGGTGTGTGAGCTGGGAGACGGCTGCGCTCAGAGGAACAAGCCAGGCGTGTACACAAGGCTCCC
F Q A F C C S W G D G C A Q R N K P G V Y T R L P 843
2551 TCTGTTTCGGGACTGGATCAAAGAGAACACTGGGGGTATAGGGCGCGGCCACCCAAATGTGTACACCTGCGGGG
L F R D W I K E N T G V (SEQ ID NO: 2) 855
2626 CCACCCATCGTCCACCCAGTGTGCACGCCCTGCAGGCTGGAGACTGGACCGCTGAC'TGCACCAGCGCCCCAGAA
2701 CATACACTGTGAACCTCAATCTCCAGGCTCCAAATCGCCTAGAAAACCTCTCGCTTCCTCAGCCTCCAAAGTGG
2776 AGCTGGAGGTAGAAGGGAGGACACTGGTGGTTCTACTGACCCCAACTGGGGCAAGGTTTGAAGACACAGCCT
2851 CCCCCGCCAGCCCAAGCTGGGCCGAGCGCGTTTGTGTATATCTGCCCTCCCCCTGTCTGTAAAGGAGCAGCGGGAA
2926 CGGAGCTTCGGAGCCTCCTCAGTGAAGTGGTGGGCTGCCGGATCTGGGCTGTGGGCCCCCTTGGGCCACGCTCT
3001 TGAGGAAGCCAGGCTCGGAGGACCCCTGGAAAACAGACGGGTCTGAGACTGAAATTTGTTTACCAGCTCCCAGGG
3076 TGGACTTCAGTGTGTATTGTGTAAATGGGTAAAAACAATTTATTTCTTTTAAAAAATAAAAAA (SEQ ID NO: 1)

____ : KOZAK'S CONSENSUS SEQUENCE
____ : TRANSMEMBRANE DOMAIN
____ : CONSERVED AMINO ACIDS OF CATALYTIC TRIAD H,D,S

Fig. 2D

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